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OM protein - protein search, using sw model

Run on: December 30, 2002, 16:15:02 ; Search time 12 Seconds

(without alignments)
224.663 Million cell updates/sec

Title: US-09-664-326-23

Perfect score: 368
Sequence: 1 LTYTCTESGQMLCEGSN.....PKQSHNDGFEEIPEYIQ 65

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	360	97.8	65 1 ITTH_HIRME	P01050 hirudo medi
2	353	95.9	65 1 ITTH_HIRME	P28506 hirudo medi
3	352	95.7	65 1 ITTH_HIRME	P28511 hirudo medi
4	350	95.1	65 1 ITTH_HIRME	P28503 hirudo medi
5	348	94.6	65 1 ITTH_HIRME	P28509 hirudo medi
6	348	94.6	65 1 ITTH_HIRME	P28508 hirudo medi
7	346	94.0	65 1 ITTH_HIRME	P28507 hirudo medi
8	345	93.8	65 1 ITTH_HIRME	P28510 hirudo medi
9	345	93.8	65 1 ITTH_HIRME	P28505 hirudo medi
10	343	93.2	65 1 ITTH_HIRME	P09945 hirudo medi
11	333	90.5	65 1 ITTH_HIRME	P09944 hirudo medi
12	315	85.6	66 1 ITTH_HIRME	P28501 hirudo medi
13	293	79.6	65 1 ITTH_HIRME	P81492 hirudinaria
14	249	67.7	63 1 ITTH_HIRME	P28512 hirudinaria
15	215	58.4	63 1 ITTH_HIRME	P28511 hirudinaria
16	173	47.0	62 1 ITTH_HIRME	P28502 hirudo medi
17	90	24.5	17 1 ITTH_HIRME	P28502 hirudo medi
18	68.5	18.6	1071 1 VARA_YEAST	P17255 saccharomyc
19	68	18.5	192 1 YADK_RHISN	P55423 rhizobium s
20	67	18.2	222 1 OS28_PLAGA	O55429 plasmodium
21	66.5	18.1	810 1 NEEL_HUMAN	O92832 homo sapien
22	66	17.9	1242 1 ZAN_RABIT	O90957 brachydanio
23	66	17.9	5376 1 ZAN_MOUSE	O88799 mus musculu
24	65.5	17.8	2700 1 ZAN_HUMAN	O94943 homo sapien
25	65	17.7	306 1 C181_HUMAN	O15165 homo sapien
26	64	17.4	317 1 IBP2_SHEEP	O29400 ovis aries
27	63.5	17.3	318 1 GSHB_VIRCH	O90957 brachydanio
28	63.5	17.3	474 1 VSM5_TRYBB	P26333 trypanosoma
29	63.5	17.3	755 1 COMP_RAT	P35444 rattus norv
30	63.5	17.3	1218 1 TAG1_HUMAN	P78504 homo sapien
31	63.5	17.3	1218 1 TAG1_HUMAN	O90957 homo sapien
32	63.5	17.3	1218 1 TAG1_HUMAN	O90957 homo sapien
33	63.5	17.3	2703 1 NTC2_DROME	P07207 drosophila

34	63	17.1	80 1 AFP4_RAPSA	O24331 raphanus sa
35	63	17.1	385 1 GUNE_FUSOX	P46239 fusarium ox
36	62.5	17.0	513 1 AVR2_HUMAN	P27037 homo sapien
37	62	16.8	79 1 AFP3_BRANA	O39313 brassica na
38	62	16.8	79 1 AFP3_RAPSA	O24332 raphanus sa
39	62	16.8	80 1 AFP2_ARATH	O80955 arabidopsis
40	62	16.8	80 1 AFP3_ARATH	O80954 arabidopsis
41	62	16.8	80 1 AFP4_ARATH	O91123 arabidopsis
42	62	16.8	264 1 SPRC_CABEL	P34714 caenorhabdi
43	62	16.8	2470 1 NTC2_MOUSE	O35516 mus musculu
44	62	16.8	2471 1 NTC2_HUMAN	O04721 homo sapien
45	62	16.8	2471 1 NTC2_RAT	O9q30 rattus norv

ALIGNMENTS

RESULT 1	ID	ITTH_HIRME	STANDARD;	PRT;	65 AA.
AC	P01050;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Hirudin variant-1 (Lepridin).				
OS	Hirudo medicinalis (Medicinal leech).				
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinidae; Hirudinea;				
OC	Arycnobdellidae; Hirudiniformes; Hirudinidae; Hirudo.				
OX	NCBI_TaxID=6421;				
RN	[1]				
RP	SEQUENCE.				
RA	Dodd J., Mueller H.-P., Seemuller U., Chang J.-Y.;				
RT	"The complete amino acid sequence of hirudin, a thrombin specific				
RT	inhibitor. Application of colour carboxymethylation.";				
RL	FEBS Lett. 165:180-183(1984).				
RN	[2]				
RP	SEQUENCE.				
RA	Petersen T.E., Roberts H.R., Sottrup-Jensen L., Magnusson S.;				
RA	Bagdy D.;				
RL	(in) Peeters H. (eds.);				
RL	Proteases of the biological fluids, Proc. 23th colloquium, pp.145-149,				
RN	[3]				
RP	STRUCTURE BY NMR.				
RX	MEDLINE=89274194; PubMed=2567183;				
RA	FOLKERS P.J.M., Clore G.M., Driscoll P.C., Dodd J., Koehler S.;				
RA	Gronenborn A.M.;				
RT	"Solution structure of recombinant hirudin and the Lys-47-->Glu				
RT	mutant: a nuclear magnetic resonance and hybrid distance				
RT	geometry-dynamical simulated annealing study.";				
RL	Biochemistry 28:2601-2617(1989).				
RN	[4]				
RP	STRUCTURE BY NMR OF 1-51.				
RX	MEDLINE=93116062; PubMed=1335515;				
RA	Szyeperski T., Guentert P., Stone S.R., Wuehrlich K.;				
RT	"Nuclear magnetic resonance solution structure of hirudin(1-51) and				
RT	comparison with corresponding three-dimensional structures determined				
RT	using the complete 65-residue hirudin polypeptide chain.";				
RL	J. Mol. Biol. 228:1193-1205(1992).				
CC	-1- FUNCTION. HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE				
CC	INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-				
CC	THROMBIN. THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.				
CC	-1- PHARMACEUTICAL: Available under the name Refludan (Hoechst Marion				
CC	Roussel). Used to treat heparin-induced thrombocytopenia (HIT).				
CC	-1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.				
CC	-1- DATABASE: NAME=Refludan; NOTE=Clinical information on Refludan;				
CC	WWW="http://www.refludan.com/".				
CC	PIR; A01289; HDLXH.				
DR	PDB; 2HIR; 15-JAN-90.				
DR	PDB; 4HIR; 15-JAN-90.				
DR	PDB; 5HIR; 15-JAN-90.				
DR	PDB; 6HIR; 15-JAN-90.				
DR	PDB; 1HIC; 31-JAN-94.				

DR PDB: 1HAG; 20-DEC-94.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR Prodom: PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family;
 KW Pharmaceutical; 3D-structure.
 FT DISULFID 6 14
 FT DISULFID 16 28
 FT DISULFID 22 39
 FT MOD_RES 63 63
 FT STRAND 5 5
 FT TURN 9 10
 FT STRAND 11 12
 FT STRAND 15 17
 FT TURN 18 19
 FT STRAND 20 21
 FT TURN 24 25
 FT STRAND 26 29
 FT STRAND 38 41
 FT STRAND 45 46
 SQ SEQUENCE 65 AA; 6970 MW; 9085A5876E3DE9PF CRC64;

Query Match 97.8%; Score 360; DB 1; Length 65;
 Best Local Similarity 96.9%; Pred. No. 2e-32;
 Matches 63; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVTYDCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEERIP 60
 : |||||
 DB 1 VYITCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEERIP 60
 OY 61 EYELQ 65
 : |||||
 DB 61 EYELQ 65

RESULT 2
 ITHK_HIRME STANDARD; PRT; 65 AA.
 AC P28506;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIb.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-90005945; Pubmed-2792365;
 RA Scharf M., Engels J., Tripler D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSSP: P09945; 4HTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR Prodom: PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14
 FT DISULFID 16 28
 FT DISULFID 22 39
 FT MOD_RES 63 63
 SQ SEQUENCE 65 AA; 6985 MW; 8F7AEAE55EA30913 CRC64;

Query Match 95.9%; Score 353; DB 1; Length 65;

Best Local Similarity 93.8%; Pred. No. 1.1e-31;
 Matches 61; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVTYDCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEERIP 60
 : |||||
 DB 1 VYITCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEERIP 60
 OY 61 EYELQ 65
 : |||||
 DB 61 EYELQ 65

RESULT 3
 ITHK_HIRME STANDARD; PRT; 65 AA.
 AC P28511;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIb.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-90005945; Pubmed-2792365;
 RA Scharf M., Engels J., Tripler D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSSP: P01050; 1HTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; HIRUDIN.
 DR Prodom: PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14
 FT DISULFID 16 28
 FT DISULFID 22 39
 FT MOD_RES 63 63
 SQ SEQUENCE 65 AA; 6968 MW; 85FD9E1AE3DE9PF CRC64;

Query Match 95.7%; Score 352; DB 1; Length 65;
 Best Local Similarity 93.8%; Pred. No. 1.4e-31;
 Matches 61; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVTYDCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEERIP 60
 : |||||
 DB 1 VYITCTESGONLCLCEGSSNVCGGKNCILGSDGKKNOCVTGEGTPKPSHNDGDFEERIP 60
 OY 61 EYELQ 65
 : |||||
 DB 61 EYELQ 65

RESULT 4
 ITHK_HIRME STANDARD; PRT; 65 AA.
 AC P28503;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIA.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.

RA MEDLINE=90005945; PubMed=2792365;
RA Scharf M., Engels J., Triplier D.;
RT "Primary structures of new 'iso-hirudins'.
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR PIR; S05673; S05673.
DR HSSP; P09945; 4HTC.
DR InterPro; IPR000429; Hirudin.
DR Pfam; PF00713; Hirudin; 1.
DR PRINTS; PR00777; HIRUDIN.
DR PRODOM; PD004216; Hirudin; 1.
KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 39 BY SIMILARITY.
FT MOD_RES 63 63 SUFFATION (BY SIMILARITY).
SQ SEQUENCE 65 AA; 6987 MW; 817E1541CF53C73 CRC64;

Query Match 95.1%; Score 350; DB 1; Length 65;
Best local Similarity 93.8%; Pred. No. 2.3e-31;
Matches 61; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LITTDCTESGONLCLCGSNVCGGNKCIIGSGEKNQCVTGEGTPKQSHNDGDFEIP 60
:|||||
DB 1 IYVTDCTESGONLCLCGSNVCGGNKCIIGSGEKNQCVTGEGTPKQSHNDGDFEIP 60

QY 61 EYVLQ 65
|||||
DB 61 EYVLQ 65

RESULT 5

ITHD_HIRME STANDARD; PRT; 65 AA.
ID ITHD_HIRME
AC P28504;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hirudin II.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_Taxid=6421;
RN [1]
RP SEQUENCE.

RA MEDLINE=90005945; PubMed=2792365;
RA Scharf M., Engels J., Triplier D.;
RT "Primary structures of new 'iso-hirudins'.
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR HSSP; P09945; 4HTC.
DR InterPro; IPR000429; Hirudin.
DR Pfam; PF00713; Hirudin; 1.
DR PRINTS; PR00777; HIRUDIN.
DR PRODOM; PD004216; Hirudin; 1.

KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 39 BY SIMILARITY.
FT MOD_RES 63 63 SUFFATION (BY SIMILARITY).
SQ SEQUENCE 65 AA; 6986 MW; 757EAE35FAEB27E CRC64;

Query Match 94.6%; Score 348; DB 1; Length 65;
Best local Similarity 92.3%; Pred. No. 3.8e-31;
Matches 60; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 LITTDCTESGONLCLCGSNVCGGNKCIIGSGEKNQCVTGEGTPKQSHNDGDFEIP 60

DB 1 IYVTDCTESGONLCLCGSNVCGGNKCIIGSGEKNQCVTGEGTPKQSHNDGDFEIP 60
:|||||
QY 61 EYVLQ 65
|||||
DB 61 EYVLQ 65

RESULT 6

ITHD_HIRME STANDARD; PRT; 65 AA.
ID ITHD_HIRME
AC P28509;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hirudin III.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_Taxid=6421;
RN [1]
RP SEQUENCE.

RA MEDLINE=90005945; PubMed=2792365;
RA Scharf M., Engels J., Triplier D.;
RT "Primary structures of new 'iso-hirudins'.
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR PIR; S05676; S05676.
DR HSSP; P01050; 1HTC.
DR InterPro; IPR000429; Hirudin.
DR Pfam; PF00713; Hirudin; 1.
DR PRINTS; PR00777; HIRUDIN.
DR PRODOM; PD004216; Hirudin; 1.

KW Serine protease inhibitor; Sulfation; Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 39 BY SIMILARITY.
FT MOD_RES 63 63 SUFFATION (BY SIMILARITY).
SQ SEQUENCE 65 AA; 7027 MW; 058E1F76B3DE9FC CRC64;

Query Match 94.6%; Score 348; DB 1; Length 65;
Best local Similarity 93.8%; Pred. No. 3.8e-31;
Matches 61; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LITTDCTESGONLCLCGSNVCGGNKCIIGSGEKNQCVTGEGTPKQSHNDGDFEIP 60
:|||||
DB 1 VYVTDCTESGONLCLCGSNVCGGNKCIIGSGEKNQCVTGEGTPKQSHNDGDFEIP 60

QY 61 EYVLQ 65
|||||
DB 61 EYVLQ 65

RESULT 7

ITHD_HIRME STANDARD; PRT; 65 AA.
ID ITHD_HIRME
AC P28508;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hirudin IIA.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_Taxid=6421;
RN [1]
RP SEQUENCE.

RA MEDLINE=90005945; PubMed=2792365;
RA Scharf M., Engels J., Triplier D.;
RT "Primary structures of new 'iso-hirudins'.
RL FEBS Lett. 255:105-110(1989).
CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR HSSP; P09945; 4HTC.
DR InterPro; IPR000429; Hirudin.
DR Pfam; PF00713; Hirudin; 1.
DR PRINTS; PR00777; HIRUDIN.
DR PRODOM; PD004216; Hirudin; 1.

RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR HSSP: P01050: 1HTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; Hirudin.
 DR ProDom: PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14 BY SIMILARITY.
 FT DISULFID 16 28 BY SIMILARITY.
 FT DISULFID 22 39 BY SIMILARITY.
 FT MOD_RES 63 63 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 65 AA; 6973 MW; CABBR0D72B6449E4 CRC64;

Query Match 94.0%; Score 346; DB 1; Length 65;
 Best Local Similarity 90.8%; Pred. No. 6.3e-31;
 Matches 59; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 LVYDTCTESGNNLCLCEGSNNVCGGCKNCLIGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 : |||||
 Db 1 VYDTCTESGNNLCLCEGSNNVCGGCKNCLIGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 |||||
 OY 61 EYLIQ 65
 |||||
 Db 61 EYLIQ 65

RESULT 8
 ITHG_HIRME STANDARD; PRT; 65 AA.
 AC P28507;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIa.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR PIR: S05675; S05675.
 DR HSSP: P01050: 1HTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; Hirudin.
 DR ProDom: PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14 BY SIMILARITY.
 FT DISULFID 16 28 BY SIMILARITY.
 FT DISULFID 22 39 BY SIMILARITY.
 FT MOD_RES 63 63 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 65 AA; 7028 MW; 05F6A0B26A3DE9FC CRC64;

Query Match 93.8%; Score 345; DB 1; Length 65;
 Best Local Similarity 92.3%; Pred. No. 8e-31;
 Matches 60; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LVYDTCTESGNNLCLCEGSNNVCGGCKNCLIGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 : |||||
 Db 1 VYDTCTESGNNLCLCEGSNNVCGGCKNCLIGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 |||||

OY 61 EYLIQ 65
 |||||
 Db 61 EYLIQ 65

RESULT 9
 ITHG_HIRME STANDARD; PRT; 65 AA.
 AC P28510;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin IIb.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
 CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
 DR PIR: S05677; S05677.
 DR HSSP: P01050: 1HTC.
 DR InterPro: IPR000429; Hirudin.
 DR Pfam: PF00713; Hirudin; 1.
 DR PRINTS: PR00777; Hirudin.
 DR ProDom: PD004216; Hirudin; 1.
 KW Serine protease inhibitor; Sulfation; Multigene family.
 FT DISULFID 6 14 BY SIMILARITY.
 FT DISULFID 16 28 BY SIMILARITY.
 FT DISULFID 22 39 BY SIMILARITY.
 FT MOD_RES 63 63 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 65 AA; 7026 MW; 1E902A81AE3DE9FC CRC64;

Query Match 93.8%; Score 345; DB 1; Length 65;
 Best Local Similarity 92.3%; Pred. No. 8e-31;
 Matches 60; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 LVYDTCTESGNNLCLCEGSNNVCGGCKNCLIGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 : |||||
 Db 1 VYDTCTESGNNLCLCEGSNNVCGGCKNCLIGSDGKKNOCVTGEGTPKPSHNDGDFEELP 60
 |||||

OY 61 EYLIQ 65
 |||||
 Db 61 EYLIQ 65

RESULT 10
 ITHG_HIRME STANDARD; PRT; 65 AA.
 AC P28505;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hirudin II'.
 OS Hirudo medicinalis (Medicinal leech).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 CC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90005945; PubMed=2792365;
 RA Scharf M., Engels J., Tripiet D.;
 RT "Primary structures of new 'iso-hirudins'";
 RL FEBS Lett. 255:105-110(1989).
 CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
 CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-


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CC CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR HSSP; P01050; 5HR.
DR InterPro: IPR000429; Hirudin.
DR Pfam: PF00713; Hirudin; 1.
DR PRINTS: PR00777; HIRUDIN.
DR ProDom: PD04216; Hirudin; 1.
KW Serine protease inhibitor; Multigene family.
FT DISULFID 6 14
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 37 BY SIMILARITY.
FT CARBOHYD 43 43 O-LINKED (GALNAc...).
SQ SEQUENCE 63 AA; 6699 MW; 8BC2828B8C51BED CRC64;

Query Match 67.7%; Score 249; DB 1; Length 63;
Best Local Similarity 67.7%; Pred. No. 1,7e-20;
Matches 44; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

OY 1 LTYDCTSGGNLCLCESNVCVGQGNCKILCSDEGRKQCVTGEETPPKPSHNDGFEIIP 60
DB 1 :YITDCTSGGNCTLCVGSNVCGEGRKQCVTGEETPPKPSHNDGFEIIP 58
OY 61 EHYLD 65
DB 59 DEXIR 63

RESULT 15
ITH6_HIRMA STANDARD; PRT; 63 AA.
AC P28512;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hirudin p6.
OS Hirudinaria manillensis (Buffalo leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinae;
OC Atychobdellida; Hirudiniiformes; Hirudinidae; Hirudinaria.
OX NCBI_TaxID=6419;
RN [1]
RP SEQUENCE, AND STRUCTURE OF CARBOHYDRATE.
RX MEDLINE=92172851; PubMed=1540584;
RA Steiner V., Knecht R., Boersen O., Gaessmann E., Stone S.R.,
RA Raachdorf F., Schlaeppi J.-M., Maschler R.;
RT "Primary structure and function of novel O-glycosylated hirudins from
RT the leech Hirudinaria manillensis."
RL Biochemistry 31:2294-2298(1992)
CC CC -1- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.
CC -1- PFM: O-LINKED GLYCAN CONSISTS OF FUC-GAL-GALNAc TRISACCHARIDE.
CC CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
DR PIR: A42207; A42207.
DR HSSP; P01050; 5HR.
DR GlycoSuiteDB: P28512;
DR InterPro: IPR000429; Hirudin.
DR Pfam: PF00713; Hirudin; 1.
DR PRINTS: PR00777; HIRUDIN.
DR ProDom: PD04216; Hirudin; 1.
KW Serine protease inhibitor; Sulfation; Glycoprotein;
KW Multigene family.
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 16 28 BY SIMILARITY.
FT DISULFID 22 37 BY SIMILARITY.
FT CARBOHYD 43 43 O-LINKED (GALNAc...).
FT MOD_RES 61 61 /FTID-CAR_000143.
SQ SEQUENCE 63 AA; 6977 MW; 149A7369CC75A192 CRC64;

Query Match 58.4%; Score 215; DB 1; Length 63;
Best Local Similarity 60.9%; Pred. No. 7.6e-17;
Matches 39; Conservative 7; Mismatches 16; Indels 2; Gaps 1;

OY 1 LTYDCTSGGNLCLCESNVCVGQGNCKILCSDEGRKQCVTGEETPPKPSHNDGFEIIP 60

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Db	1	MRTACTESQONOCICGNDVCGGRCQFPDSSGK--CVEGSTRKPONEGQHDDPIP	58
OY	61	EEYL 64	
Db	59	EEYL 62	

Search completed: December 30, 2002, 16:17:00
Job time : 13 secs

